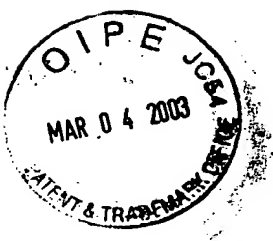




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FIG. 1A

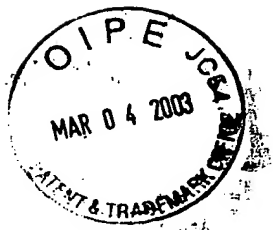
CGGGAGAATAGTGCACCAAGGGATGCCCCGTGAAATATTAATTAAACGTTTTTAAGAACA -101
TCATCAAACCCGGGCCCCCATCATGAAGGAATAACAAGGCCCTTCGAAAAGTATGGGAAACT -41
GGTCGGCAGGACATCAGCATTATTAATTCTAGGAAACTCATTATGGATAACAAGGAAACT 18
M D N K E T 6
AACGGAGAGCTAGAGCAGTCTGATGAGGCCGATCCGTCCGGTCAAAACCTTGATGATGGG 78
N G E L E Q S D E A D P S G Q N L D D G 26
GAAACCGATAGCAAACAAGAAGAGAATCTCATCAACGTTAGCCCGCCAAAAACACCGCCA 138
E T D S K Q E E N L I N V S P P K T P P 46
GGTCCTCCTCCTCCTCTAAAGAATGGAGGAAGGGGTGAGAAACCGCCCAAAATCCCAATA 198
G P P P P L K N G G R G Q K P P K I P I 66
TGTCATCAAATGGAAAGCTCCCCAAGGAAGTTGAATGGACAGAAGACAGAGGGCGAAGAC 258
C H Q N G K L P K E V E W T E D R G E D 86
AGAAAGGATAGTCTCACTCTTCAATCAAAGCTAGATCACGGGGCATAACGGATGAGAAA 318
R K D S L T L Q S K L D H G A Y T D E K 106
CAGGATCTTCTAACATATCTTGACCGTCACGGCATCAACAGTCCAGTCAAGCTAACACCA 378
Q D L L T Y L D R H G I N S P V K L T P 126
GATGAAACTGGAGGGAGCAGTGCTTTGGATATTCTTGGGATTATTGAAGAGAGGGACACT 438
D E T G G S S A L D I L G I I E E R D T 146
GGTGCACCTAGGCTCTGATCCCTCATCCACTATGCAGGCCATGGCTAAACCTGTAGGCTTT 498
G A L G S D P S S T M Q A M A K P V G F 166
CTGCAGAGGCAGCTATGGACTGTCTCCAACCTTCAGACAATAGACTCTCCATGAAACTT 558
L Q R Q L W T V L Q P S D N R L S M K L 186
TTCGGAAGCAAGAAAGGGTTACAAAAGGAAAAATATCGGCTGAGGAAGGCGGGGTTCTT 618
F G S K K G L Q K E K Y R L R K A G V L 206
ATCATTTCATCCATGTAGTCATTTTCAGATTTTACTGGGATCTACTGATGCTGTGCCTGATC 678
I I H P C S H F R F Y W D L L M L C L I 226
ATGGCAAACGTCATCCTCCTACCCGTCGTCATTACTTTCTTCCACAACAAGGACATGAGT 738
M A N V I L L P V V I T F F H N K D M S 246
ACGGGTTGGCTCATCTTTAATTGCTTCTCAGATACCTTCTTCATTCTCGATCTCATCTGC 798
T G W L I F N C F S D T F F I L D L I C 266
AACTTTCGGACCGGCATCATGAATCCGAAGTCGGCCGAACAGGTGATCCTCAACCCCCGT 858
N F R T G I M N P K S A E Q V I L N P R 286
CAAATCGCCTATCATTATCTCCGTTTCATGGTTCATCATCGATCTCGTGTCTTCCATCACC 918
Q I A Y H Y L R S W F I I D L V S S I P 306



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FIG. 1A (Continued)

ATGGACTACATCTTCCTCCTCGCTGGCGGCCAGAACCGTCACTTCCTCGAGGTGTCCCGA	978
M D Y I F L L A G G Q N R H F L E V S R	326
<hr/>	
S4	
GCCTCAAGATACTGCGCTTTGCCAAGCTCCTCAGTCTTCTTCGACTCCTGCGTCTGTCC	1038
A L K I L R F A K L L S L L R L L R L S	346
<hr/>	
AGGCTCATGCGGTTCGTCAGTCAATGGGAACAGGCCTTCAACGTAGCCAATGCCGTCATC	1098
R L M R F V S Q W E Q A F N V A N A V I	366
<hr/>	
S5	
CGGATCTGTAATCTAGTGTGTATGATGCTTCTGATTGGCCATTGGAATGGCTGCCTTCAA	1158
R I C N L V C M M L L I G H W N G C L Q	386
<hr/>	
TATCTCGTGCCCATGCTGCAAGAATACCCCGACCAATCATGGGTGCGCCATTAATGGCCTT	1218
Y L V P M L Q E Y P D Q S W V A I N G L	406
<hr/>	
Pore	
GAGCACGCTCATTGGTGGGAGCAGTATACATGGGCACTCTTCAAAGCCCTTTCGCACATG	1278
E H A H W W E Q Y T W A L F K A L S H M	426
<hr/>	
CTCTGTATCGGGTACGGCAAGTTCCCCCTCAAAGCATCACCGATGTCTGGCTAACGATT	1338
L C I G Y G K F P P Q S I T D V W L T I	446
<hr/>	
S6	
GTCAGTATGGTGTCCGGTGGGACCTGCTTCGCCCTGTTTCATCGGACACGCTACCAATCTC	1398
V S M V S G A T C F A L F I G H A T N L	466
<hr/>	
ATCCAGTCCATGGACTCCTCCAGCAGGCAATACCGTGAGAAGTTGAAACAAGTTGAAGAG	1458
I Q S M D S S S R Q Y R E K L K Q V E E	486
<hr/>	
TACATGCAGTATCGCAAGCTACCGTCCCACCTACGAAACAAGATCCTCGATTACTACGAG	1518
Y M Q Y R K L P S H L R N K I L D Y Y E	506
<hr/>	
TACCGATACCGAGGAAAGATGTTTGATGAGAGGCATATCTTTCGAGAAGTGTCGGAGAGT	1578
Y R Y R G K M F D E R H I F R E V S E S	526
<hr/>	
ATACGACAGGATGTGCGAAACTACAATTGTGCGGACCTGGTTCGCATCCGTCCCTTTCTTC	1638
I R Q D V A N Y N C R D L V A S V P F F	546
<hr/>	
GTCGGTGCCGACTCAAACCTTCGTCACCCGTGTGGTGACGCTGCTCGAATTCGAGGTCTTC	1698
V G A D S N F V T R V V T L L E F E V F	566
<hr/>	
CAACCCGCTGACTATGTTATACAGGAAGGTACTTTTCGGTGATCGCATGTTCTTCATCCAG	1758
Q P A D Y V I Q E G T F G D R M F F I Q	586
<hr/>	
CAGGGCATCGTCGACATCATCATGTCCGACGGCGTCATCGCCACGTCACTCAGTGACGGC	1818
Q G I V D I I M S D G V I A T S L S D G	606
<hr/>	
cNMP binding site	
TCATATTTTGGCGAAATCTGCCTGCTTACCCGTGAGCGCCGCGTGGCATCGGTGAAGTGC	1878
S Y F G E I C L L T R E R R V A S V K C	626
<hr/>	
GAGACCTACTGCACGCTCTTCTCGCTCTCCGTCCAGCATTTCAACCAAGTGCTCGACGAG	1938
E T Y C T L F S L S V Q H F N Q V L D E	646



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FIG. 1A (Continued)

TTTCCCGCCATGAGGAAAACGATGGAAGAGATAGCCGTTTCGTCTGACCCGAATCGGG 1998
F P A M R K T W E E I A V R R L T R I G 666

AAGGAATCGAGCAAGCTGAAATCCCCCCTAGAGAGCCCGACGATCAGGGGACACTGCCCT 2058
K E S S K L K S R L E S P T I R D T A P 686

CTCTTTCCGATCCCACCTGATACACCGTCTTTTCGTACCCGACATCGAAAAGAACCGGTC 2118
L F P I P P D T P S F V T D I E K N R F 706

TTTGGCGACGACACGGACGATGTACACATCAGGACCCGAGTCGACGTCGAGCGTCGTTTCG 2178
F G D D T D D V H I R T R V D V E R G S 726

CATGAAAACGTCATCGCCATCATGGATGGGAGTTTATCCGACCTCAGGATGGAAAACGAA 2238
H E N V I A I M D G S L S O L R M E N E 746

ATCCAAGCCCGTAAATCGTCTAGCGGAAAACGGAGGAAATTCAGCAACAAAACAACCGAA 2298
I Q A R K S S S G K R R K F Q Q Q T T E 766

CTATGACGACTTGAAACAAACAATGATGGACGCTTACAATTTCCAGTGATTCAATACTTA 2358
L - [SEQ. ID NO. 18] 767

CGCAATGCAGACATTAGCTTTTGTACCTGATTGTTTAGAATGTATTGAATTTGTAGATCA 2413

GTCCGGCAAATAAGAAAGCATAATTTGGAATTTCTTTCATTGAGGAAGTACTGAAAACAA 2478

TGTGATAGCAGCCGGTAGAAATTTCTTGTCCATTATCGAGCCTATATTTTTCGCGCTTTC 2538

TTACGAAGTAAATGAAAGGATCAATTAATTTATTGTTCTTTGTCTCGTCCGCTTTGTATC 2598

TGATGCCGAAAAGGAATGAAACGTGATTAGAACAGTAATCGATTGAACTACAGAAGTCTT 2658

TTCAAAATGTTGAATGTATGAAGGAGGAGGGGAAGGTTTGATATATGCAAAGAAATGGA 2718

GAAATATTTTGTAAATTTATCTAGAATGGTACTATTGATGCTGGAAAGGTGTTGAAGTT 2778

GTCCAATATTGTGTCAAATCACCAACTATTTGACATTTGTCTTTTTC [SEQ. ID NO. 4] 2825

FIG. 1C

pore

416.	T	N	A	L	F	K	A	S	H	M	L	C	I	G	Y	G	K	F	P	P	O	S	-418
418.	P	D	A	F	W	A	V	T	M	T	T	T	V	G	Y	G	D	M	T	P	V	G	-440
441.	V	T	A	L	F	T	T	T	C	M	T	S	V	G	G	N	V	A	A	T	T	T	-463
612.	V	T	A	L	F	T	F	S	S	L	T	S	V	G	G	N	V	S	P	N	T	T	-634
248.	V	T	A	L	W	S	T	T	T	L	T	T	T	T	G	Y	G	D	F	H	T	N	-270
348.	V	T	A	L	W	S	T	T	L	T	T	T	T	T	I	G	-	E	T	P	P	P	-368

FIG. 1B

S4 motif

SPIH	326-	R	A	L	K	I	L	R	F	A	K	L	L	S	L	L	R	L	L	R	L	S	R	L	M	R	-350	
Shaker	344-	M	S	L	A	I	L	R	V	I	R	L	V	R	V	F	R	I	F	K	L	S	R	H	S	K	-368	
DmEAG	341-	S	L	F	S	A	L	K	V	V	R	L	L	R	L	G	R	V	V	R	K	L	D	R	Y	L	-365	
HERG	519-	E	L	I	G	L	L	K	T	A	R	L	L	R	L	V	R	V	A	R	K	L	D	R	Y	S	-343	
KAT 1	168-	S	M	L	R	L	W	R	L	R	L	R	V	S	S	L	F	A	R	L	E	K	D	I	R	F	N	-192
brCNGC α	263-	W	N	Y	P	E	I	R	L	N	R	L	L	R	I	S	R	M	F	E	F	F	Q	R	T	E	-287	

FIG. 1D

cNMP binding domain

	533-F	485-L	462-L	579-C	750-C	143-E	110-Q	10-T
SPIH	U L L E F E V F Q P	D Y V I Q E G T F G D R M F F I	Q Q G I V D I I	D	G V A A	T S L S D G S Y F G E I		
brCNGC α	L V E P V L K L P P V S P	D Y C K K G D I G R E N	I I K E C K A V V A D D		G T Q F V V	L S D G S Y F G E I		
boCNGC α	L V E P V L K L R P V F S P	D Y C R K G D I G K E N	I I K E G K A V A D D		G V T Q Y	L L S A G S C F G E I		
DmEAG	C R A A M H F M S H S A P	D L Y H T G E S I D S C F I V T G S	S H I Q Q D D		E V A A	I L R K G D V F G Q		
HERG	C R A A M K F K T T H A P P	D T H A G D L L T A	F I S R G S	E I A R D	V V A A	I L R K N D I F G E P		
PKA I	E R S D F D A F P V S E I	T V I Q G D E G D N F	V I Q G E D	V Y M N E		W A T S	G G S F G E I	
PKG I	Q E A U D C Y P V E	G K D S C I K E G D V G S L	V M G K V	E Y T K E		G V K L C D	E G P G K V F G E I	
CAP	E W F L H C H I N K	P S K S T I I H G E K A	T M I V K G S V A	D K D E E G K E N	I L S Y I N G D	I G E I		

[illegible]

FIG. 2A

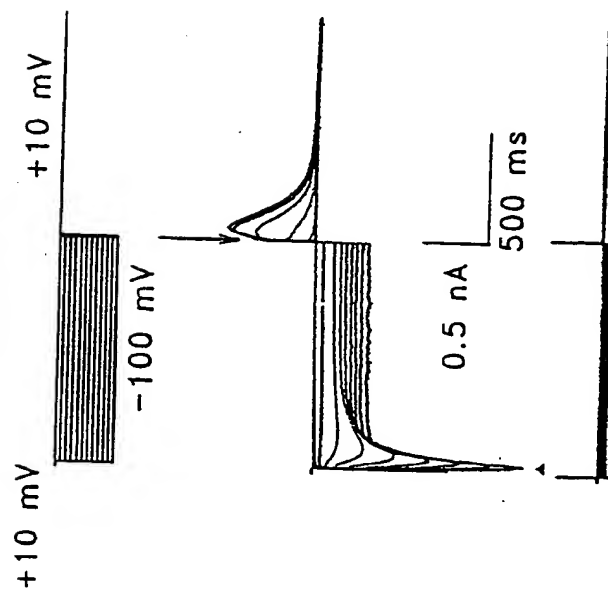


FIG. 2B

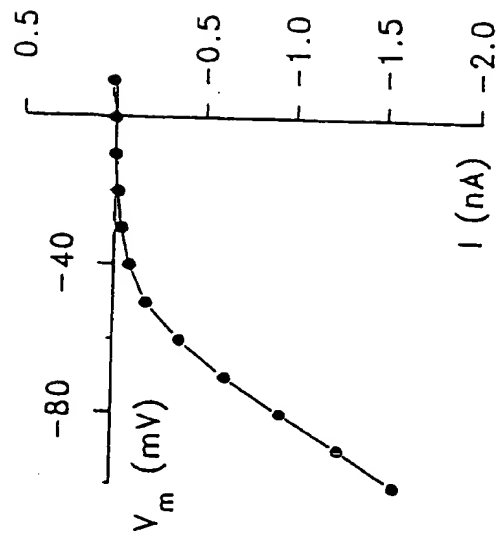


FIG. 2C

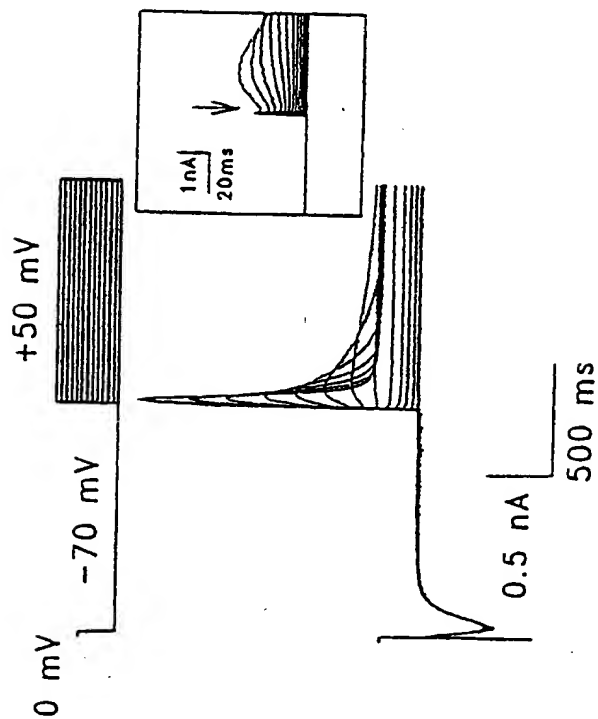


FIG. 2D

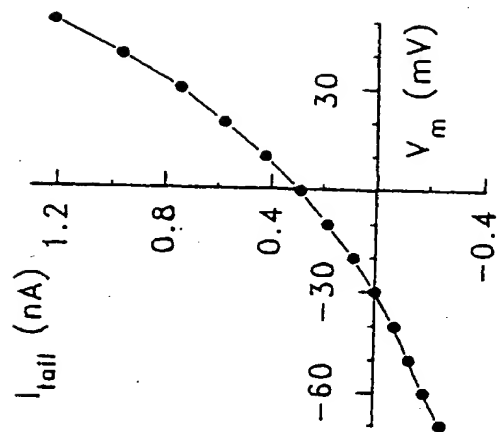


FIG. 2E

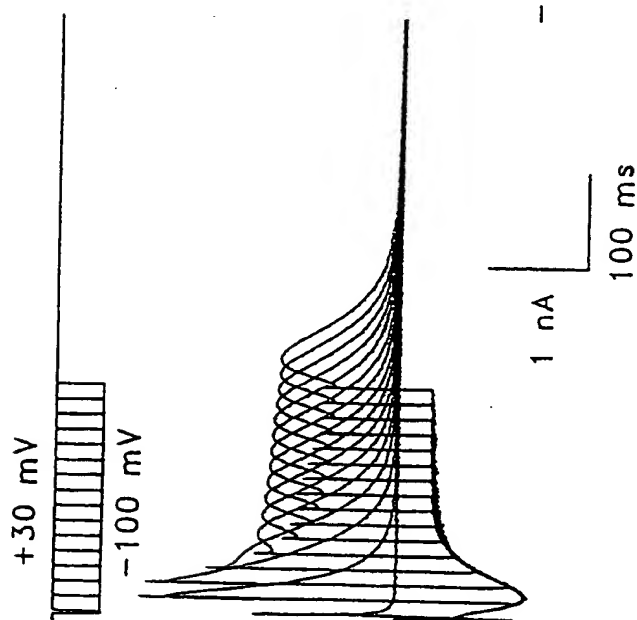
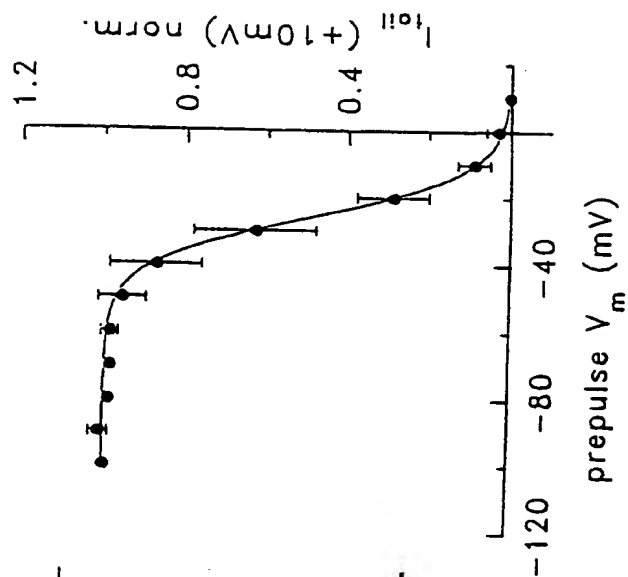


FIG. 2F



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FIG. 3A

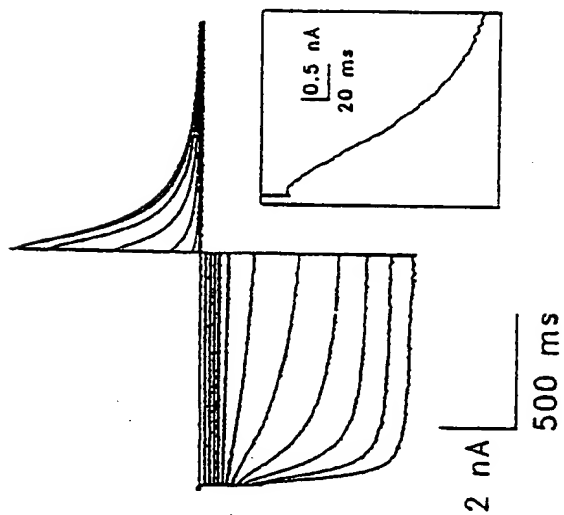
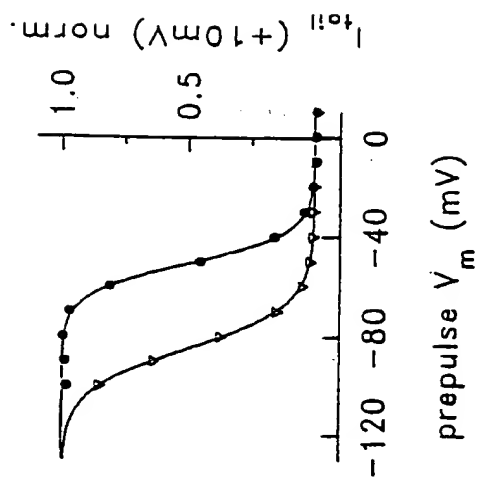


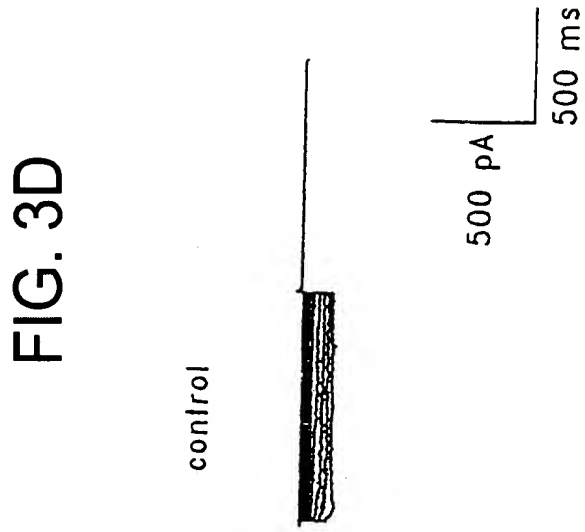
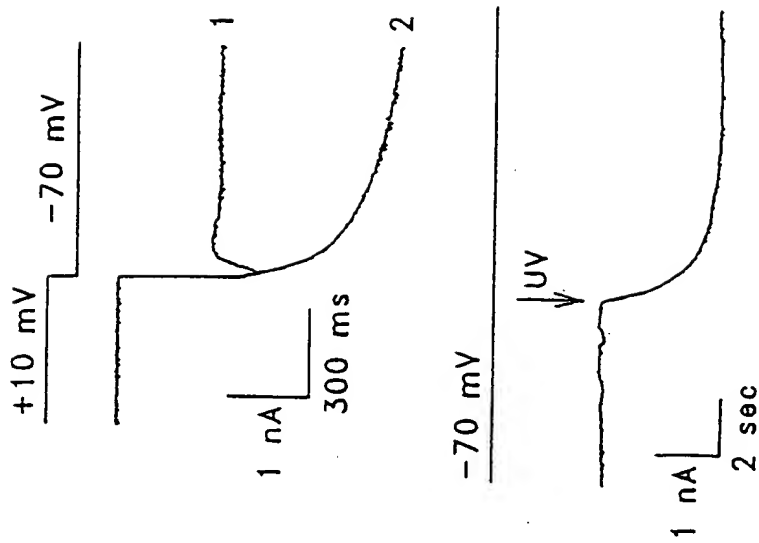
FIG. 3B

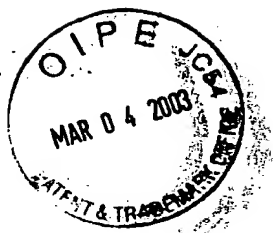




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FIG. 3C





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FIG. 3F

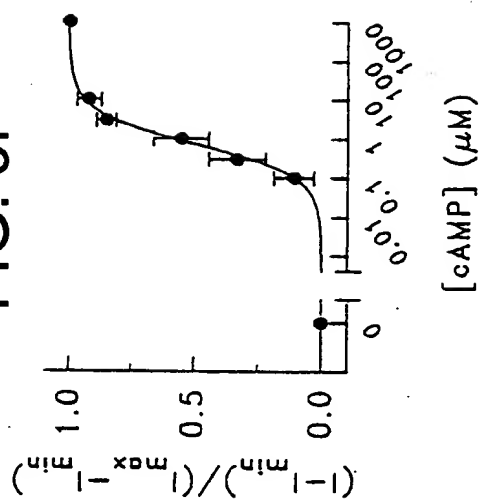
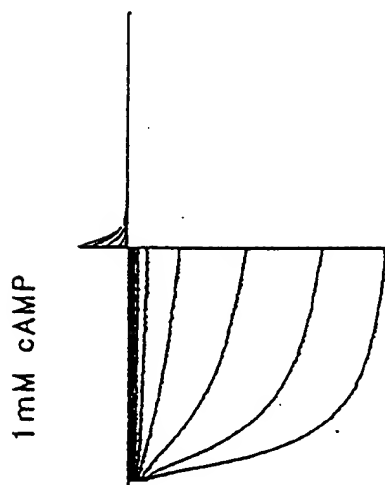


FIG. 3E



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FIG. 4A

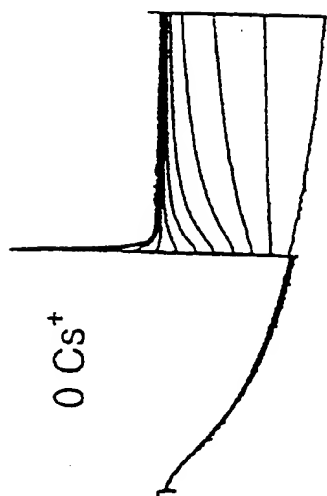


FIG. 4B

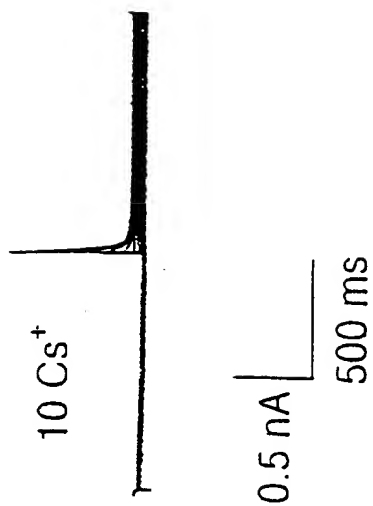


FIG. 4C

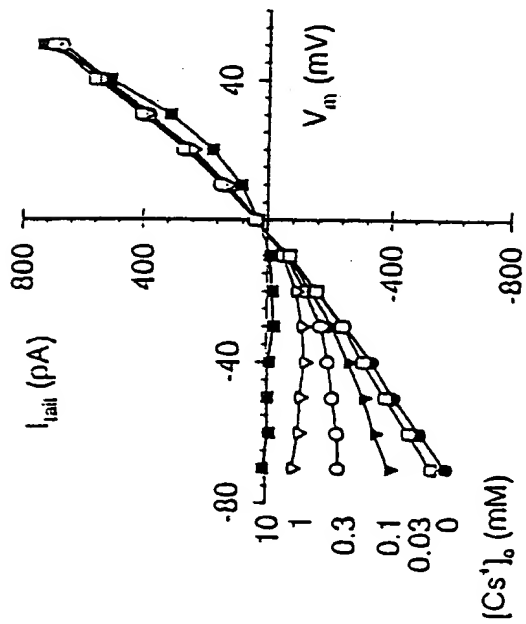


FIG. 4D

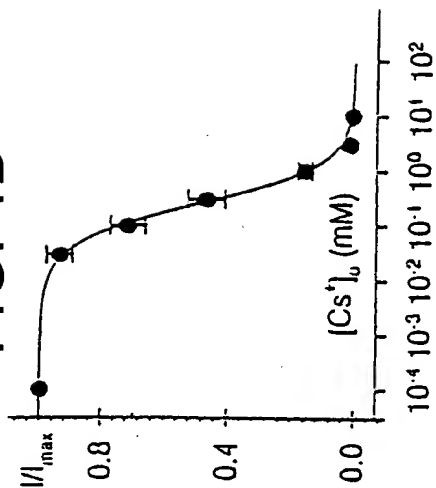
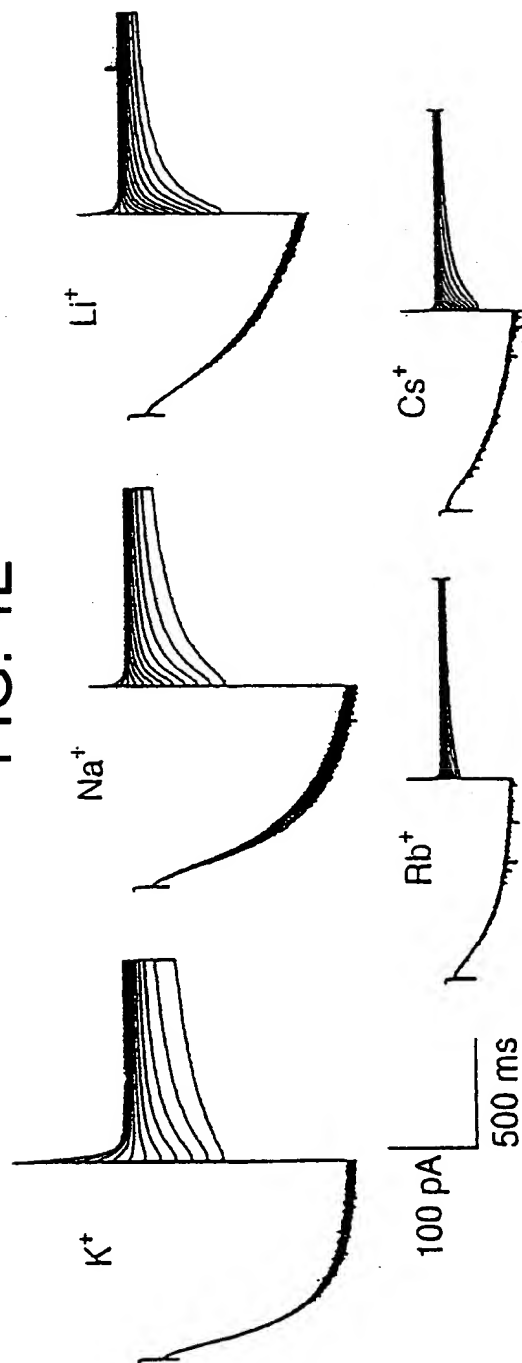


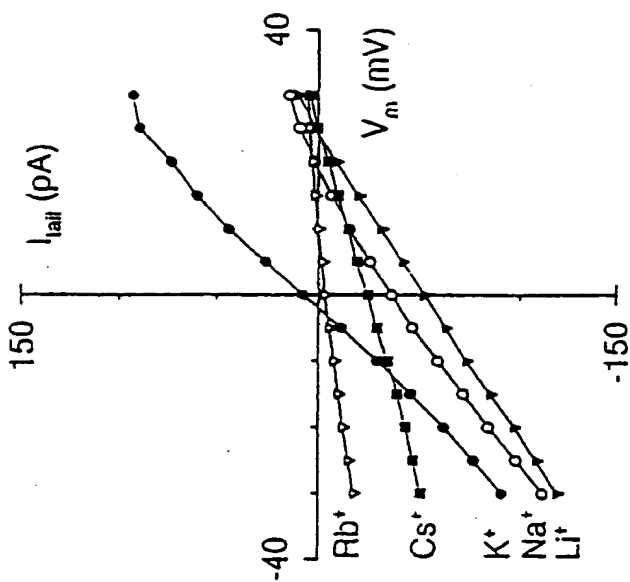
FIG. 4E





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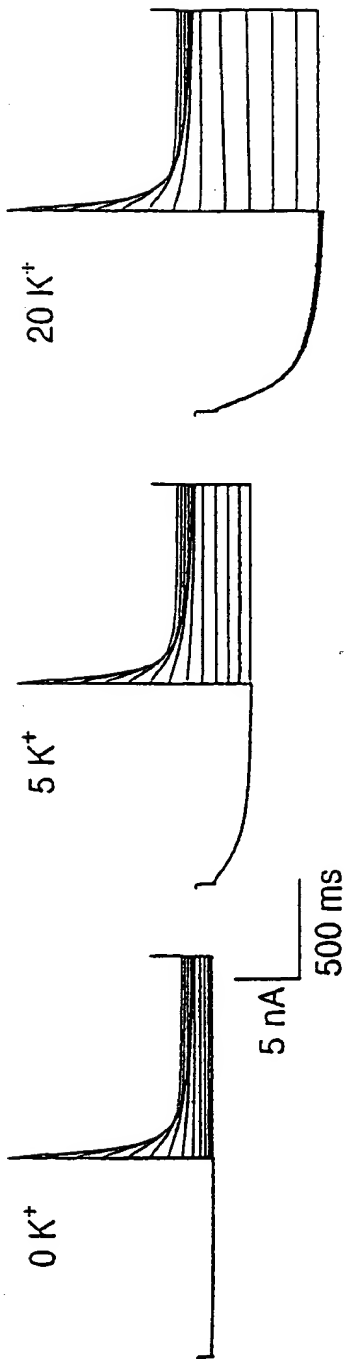
FIG. 4F





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FIG. 4G





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FIG. 4H

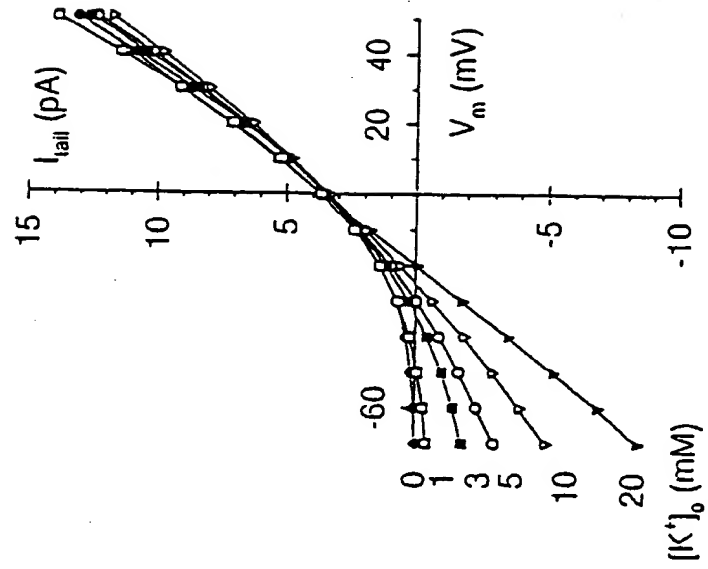




FIG. 5A

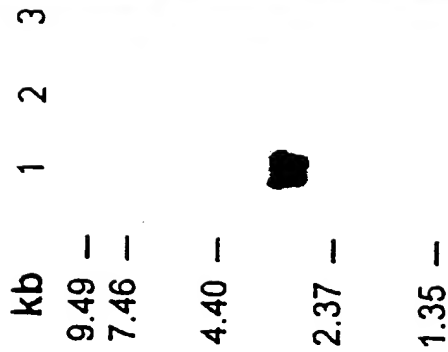


FIG. 5B

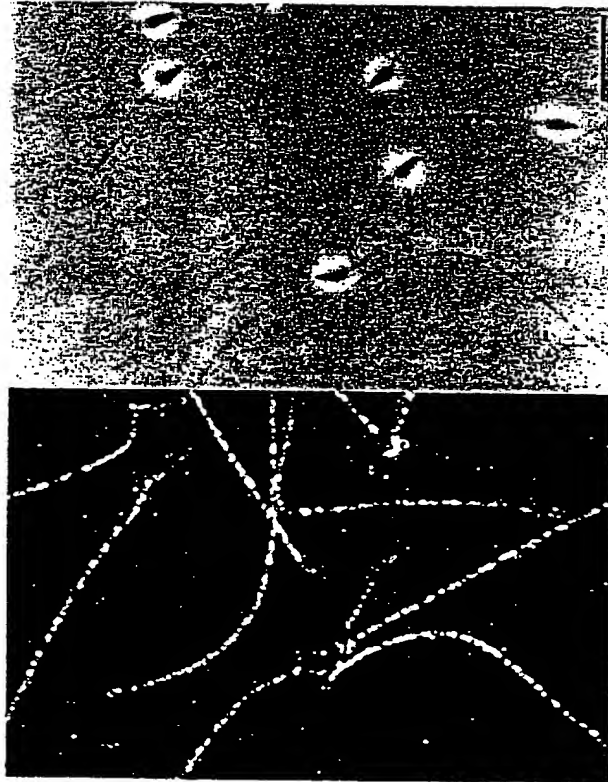
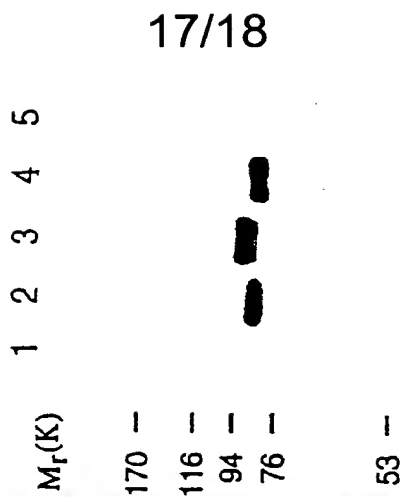


FIG. 5C





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FIG. 6

